

STIC-ILL

NPL

From: Swope, Sheridan
Sent: Monday, March 03, 2003 8:11 PM
To: STIC-ILL
Subject: 09917376

GREETINGS!!!

I need copies of:

Tomme P et al 1995, in Enzymatic Degradation of Insoluble Polysaccharides (Saddler and Penner, eds) at 142-163, American Chemical Society, Washington.

Gilkes NR, Warren RA, Miller RC Jr, Kilburn DG.

Precise excision of the cellulose binding domains from two *Cellulomonas fimi* cellulases by a homologous protease and the effect on

catalysis.

J Biol Chem. 1988 Jul 25;263(21):10401-7.

THANKS!!!

Sheridan Swope, Ph.D.
Patent Examiner, AU 1652
Recombinant Enzymes
sheridan.swope@uspto.gov
703-305-1696 (voice)
703-308-3014 (FAX)
Mailbox: CM1 Rm10D01
Office: CM1 Rm12D12

General	Description	References	Links	Sequence
---------	-------------	------------	-------	----------

General information

Entry name	O74170
Accession number	O74170
Created	TrEMBLrel. 08, 1-NOV-1998
Sequence update	TrEMBLrel. 08, 1-NOV-1998
Annotation update	TrEMBLrel. 22, 1-OCT-2002

Description and origin of the Protein

Description	Avicelase III.
Gene name(s)	AVIII.
Organism source	Aspergillus aculeatus.
Taxonomy	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI TaxID	5053

References

[1]	Arai,M., Takada,G., Kawaguchi,T., Sumitani,J., Avicelase III from Aspergillus aculeatus.Submitted JUN-1998 to the EMBL GenBank DDBJ databases
	Position SEQUENCE FROM N.A.

Database cross-references

EMBL	AB015511; BAA29031.1; -.
HSSP	P00725; 2CBH.
InterPro	IPR000254; CBD_fungal. IPR002860; GH_BNR.
Pfam	PF02012; BNR; 7. PF00734; CBM_1; 1.
ProDom	PD001821; CBD_fungal; 1.
SMART	SM00236; fCBD; 1.
PROSITE	PS00562; CBD_FUNGAL; 1.

Sequence information

Length: 856 aa, molecular weight: 89820 Da, CRC64 checksum: BE085983AF60ED76

MARSSLALLC	AALLGKLADA	AASQAYTWKN	VVTGGGGGFT	PGIVFNPSAK	GVAYARTDIG	60
GAYRLNSDDT	WTPLMDWVGN	DTWHDWGIDA	LATDPVDTR	VYVAVGMYTN	EWDPNVGSIL	120
RSTDQGDWT	ETKLPFKVGG	NMPGRGMGER	LAVDPNKNSI	LYFGARSGHG	LWKSTDYGAT	180
WSNVTSFTWT	GTTFQDSSST	YTSDPVGIWA	VTFDSTSGSS	GSATPRIFVG	VADAGKSVFK	240
SEDAGATWAW	VSSEPQYGFL	PHKGVLSPPE	KTLYISYANG	AGPYDGTNGT	VHKYNITSGV	300
WTDISPTSLA	STYYGYGGLS	VDLQVPGTLM	VAALNCWWPD	ELIFRSTDG	ATWSPIEWWN	360
GYPISINYYYS	YDISNAPWIQ	DTTSTDQFPV	RVGWMVEALA	IDPFDSNHWL	YGTGLTVYGG	420
HDLTNWDSKH	NVTVKSLAVG	IEEMAVLGLI	TPPGGPALLS	AVGDDGGFYH	SLLDAAPNQA	480
YHTPTYGTTN	GIDYAGNKPS	NIVRSGASDD	YPTLALSSNF	GSTWYADYAA	STSTGTGAVA	540
LSADGDTVLL	MSSTSGALVS	KSQGTLTAVS	SLPSGAVIAS	DKSDNTVFG	GSAGAIYVSK	600
NTATSFTKT	SLGSSTTVNA	IRAHPSIAGD	VWASTDKGLW	HSTDYGSTFT	QIGSGVTAGW	660

SFGFGKASST GSYVVIYGFF TIDGAAGLFK SEDAGTNWQV ISDASHGFGS GSANVVNGDL 720
QTYGRVFRGH ERPGHLLRQS QREPAGRHD GDGDTTTSKT STTVSTTLKT TTSSASTTSS 780
STTVKTTTSS SSTTSKASST TTTKTTTTST TTSSGTTATA SAYAOCGGNG WTGATVCFTG 840
YTCTYSNAFY SQCVPS 856

//

CBD


General	Description	References	Links	Sequence
---------	-------------	------------	-------	----------

```

ID  CBD_FUNGAL; PATTERN.
AC  PS00562;
DT  DEC-1991 (CREATED); NOV-1997 (DATA UPDATE); JUL-1998 (INFO UPDATE).
DE  Cellulose-binding domain, fungal type.
PA  C-G-G-x(4,7)-G-x(3)-C-x(5)-C-x(3,5)-[NHG]-x-[FYWM]-x(2)-Q-C.
NR  /RELEASE=40.7,103373;
NR  /TOTAL=22(19); /POSITIVE=22(19); /UNKNOWN=0(0); /FALSE_POS=0(0);
NR  /FALSE_NEG=1; /PARTIAL=0;
CC  /TAXO-RANGE=??E??; /MAX-REPEAT=4;
CC  /SITE=1,disulfide; /SITE=7,disulfide; /SITE=9,disulfide;
CC  /SITE=16,disulfide;
DR  Q00023, CEL1_AGABI, T; Q12714, GUN1_TRILO, T; P07981, GUN1_TRIRE, T;
DR  P07982, GUN2_TRIRE, T; Q12624, GUN3_HUMIN, T; P43317, GUN5_TRIRE, T;
DR  P46236, GUNB_FUSOX, T; P46239, GUNF_FUSOX, T; P45699, GUNK_FUSOX, T;
DR  P15828, GUX1_HUMGR, T; Q06886, GUX1_PENJA, T; P13860, GUX1_PHACH, T;
DR  P00725, GUX1_TRIRE, T; P19355, GUX1_TRIVI, T; Q92400, GUX2_AGABI, T;
DR  P07987, GUX2_TRIRE, T; P49075, GUX3_AGABI, T; P46238, GUXC_FUSOX, T;
DR  P50272, PSBP_PORPU, T;
DR  O59843, GUX1_ASPAC, N;
3D  1AZ6; 1AZH; 1AZK; 1CBH; 2CBH;
DO  PDOC00486;
//

```

S G G - x(12) - G - x(42) - G - x(8) - N - x(5) - G - x

 ExPASy Home page	Site Map	Search ExPASy	Contact us	PROSITE
Search	<input type="text" value="Swiss-Prot/TrEMBL"/>	▼	for <input type="text"/>	<input type="button" value="Go"/> <input type="button" value="Clear"/>

Search in PROSITE for: glycosyl hydrolase family 74

(Release 17.38, of 23-Feb-2003)

*No data on
consensus sequence*

Enter search keywords:

☐ Prefix and append wildcard '*' to words.

By default, this search engine searches for complete words only. If you did not find what you expected, and would try to do a substring match, you should perform a new search and select 'prefix and append wildcard to words'.

Warning: The search for adjacent words is performed for only two words.
The request is performed as:
glycosyl hydrolase AND hydrolase family AND family 74

No PROSITE document found. Please try again.




 ExPASy Home page	Site Map	Search ExPASy	Contact us	PROSITE
--	--------------------------	-------------------------------	----------------------------	-------------------------

InterPro

[Sequence Search](#)...or text search :

InterPro Entry IPR003305

Carbohydrate-binding, CenC-like

Database	InterPro
Accession	IPR003305; CBM_CenC (matches 97 proteins)
Name	Carbohydrate-binding, CenC-like
Type	Domain 
Dates	14-NOV-2000 (created) 12-FEB-2001 (last modified)
Signatures	PF02018; CBM_4_9 (97 proteins)
Abstract 	<p>The 1,4-beta-glucanase CenC from <i>Cellulomonas fimi</i> contains two cellulose-binding domains, CBD(N1) and CBD(N2), arranged in tandem at its N-terminus. These homologous CBDs are distinct in their selectivity for binding amorphous and not crystalline cellulose [1]. Multidimensional heteronuclear nuclear magnetic resonance (NMR) spectroscopy was used to determine the tertiary structure of the 152 amino acid N-terminal cellulose-binding domain from <i>Cellulomonas fimi</i> 1,4-beta-glucanase CenC (CBDN1)[2]. The tertiary structure of CBDN1 is strikingly similar to that of the <u>bacterial</u> 1,3-1,4-beta-glucanases, as well as other sugar-binding proteins with jelly-roll folds.</p>
Examples	<ul style="list-style-type: none">• Q53317 XYND_RUMFL• P40944 XYNA_CALSR• Q05156 GUN1_STRRE• P14090 GUNC_CELFI• Q05638 CHIX_STROI View examples
References	<ol style="list-style-type: none">1. Brun E., Johnson P.E., Creagh A.L., Tomme P., Webster P., Haynes C.A., McIntosh L.P. <i>Structure and binding specificity of the second N-terminal cellulose-binding domain from Cellulomonas fimi endoglucanase C.</i> Biochemistry 39(10): 2445-2458(2000). [MEDLINE:20170870]2. Johnson P.E., Joshi M.D., Tomme P., Kilburn D.G., McIntosh L.P. <i>Structure of the N-terminal cellulose-binding domain of Cellulomonas fimi CenC determined by nuclear magnetic resonance spectroscopy.</i> Biochemistry 35(45): 14381-14394(1996). [MEDLINE:97074498]
Matches 	Table all Graphical all Condensed graphical view

O42181/201-285 YVACIKESSSSGGGAERSELYIESSTPCNITR.EQ@NSVCFITASHRYGGLGGRHEGLCTNSI
O08852/180-261 YVACLPDNSSGAVAA...V.PHYFAHEGPLET.EAGSAFCFSAGEGLAALSEQNOCLCGAGQA
PKD1_HUMAN/180-261 YVACLPDNSSGTMAA...V.SFSAAHEGLIOP.EAGSAFCFSTGQGLAALSEQGWCLCG/
Q12215/42-122 YEGCY...SAADIQS...A.GLSIKNSYIYQSVSYCQNOCP..ESAVVALFNGSDCYCGNSVSFLT
YN23_YEAST/28-108 YKACY...SASDIRK...L.GLTYKGVYIYQSVSYCQNECP..GOAVVALFNGTGCYCGGSV
YLU2_PICAN/18-91 YLGCY...SSDAIS.....GLTKKDSYTWOSSSHCTEQCS.GHAVAALINGQDCYCGDDVP.....
SLG1_YEAST/24-100 YVNCF.....SSLPS.....DESKADSYNWQSSSHCNSECSAKGASYFALYNHSECYCGDTNP...
YHC8_YEAST/28-99 QSVCS...SQN.....I.AITDGVRNOFQSNQWCSNNCAG...HQFAIVQCFMWCSDSEP...S
O60276/38-117 YIGCF...DDGHERT...I.KGAVFYDIERKMTVSHCQDACAERSYVYAGLEAGAEYCYCGNRLP
O14402/819-904 FLGCYS..DNVNGRT...LANOVQVAGGASAMSIEACETASESAGYTIAGVEYSGEQWCDTKF
O14402/930-1014 FRGGYT..DSVNARA...LI.AESVPNGPSSMTIEACQSVCKGLGYTLAGLEYADECYCGNSLA

O42181/201-285 CTNP...QVMEVIG
O08852/180-261 CSSISLSLNSACGG
PKD1_HUMAN/180-261 CSGPPAPPAPTORG
Q12215/42-122 CSGWPYQM...CGG
YN23_YEAST/28-108 CAGWPYQN...CGG
YLU2_PICAN/18-91 CTGYPMEK...CGG
SLG1_YEAST/24-100 CFGYSSEM...CGG
YHC8_YEAST/28-99 CPGYGYED...CGN
O60276/38-117 CKGEKGSV...CGA
O14402/819-904 CSGAPQET...CGG
O14402/930-1014 CAGNAAET...CGG

The coloured markup was created by Jalview (Michele Clamp)

Alignments are colored using the ClustalX scheme in Jalview (orange:glycine (G); yellow: Proline (P); blue: small and hydrophobic amino-acids (A, V, L, I, M, F, W); green: hydroxyl and amine amino-acids (S, T, N, Q); red: charged amino-acids (D, E, R, K); cyan: histidine (H) and tyrosine(Y)).